```
==============================================================
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Mark Spencer
Timestamp: Wed May 16 16:15:29 EDT 2007
==============================================================


*************************************************************
Reviewer Comments:
```

E254  The total number of bases conflicts with running total, Input: 22, Calculated : 17 SEQID (6710511)

E253  The number of bases differs from <211> Input: 12 Calculated:17 SEQID (6710511)


<210> 6710511
<211> 12
<212> DNA
<213> Homo sapiens


<400> 6710511
catatacctc tt      <211> 22
<212> DNA
<213> Homo sapiens


<400> 6710519
catatagcat tgataatctt ca      22


Fix – Change the number of bases to the right of sequence for 6710511 to 12.
  Missing SEQ ID # 6710512 to complete SEQ ID # 6710519.


E254  The total number of bases conflicts with running total, Input: 22, Calculated : 24 SEQID (9319192)

E253  The number of bases differs from <211> Input: 22 Calculated:24 SEQID (9319192)


<210> 9319192
<211> 22
<212> DNA
<213> Homo sapiens


<400> 9319192
aatgaaatga agatatgatc ag    1> 22
<212> DNA
<213> Homo sapiens


<400> 9319201
aatgcagtga gccattaaat gg    2

Fix – Change the number of bases to the right of sequence for 9319192 to 22.
   Missing SEQ ID # 9319193 to complete SEQ ID # 9319201.


E202        Invalid input format; Value must be an integer in <210> in SEQID (9974642)
E249        Order Sequence Error <210> -> <213>; Expected Mandatory Tag: <211> in SEQID
( 9974642 )


<210> 9974642
<211> 22
<212> DNA
<213> Homo sapiens

<400> 9974642
tctcagggct cagagctcag gc                                    22


<210> 9972> DNA
<213> Homo sapiens

<400> 9974651
tctcctgcca ctgcttccca tt                                    22


Fix – Missing SEQ ID # 9974643 to complete SEQ ID # 9974651.


E254        The total number of bases conflicts with running total Input: 0, Calculated : 20 SEQID
(10068324)
E253        The number of bases differs from <211> Input: 18 Calculated:20 SEQID (10068324)


This is OK no fix is required.


E252        Calc# of Seq. differs from actual; 10068324 seqIds defined; count=10068237

Fix – Numeric Identifier <160> says there is a total of 10068324 sequences. The computer only counted 10068237.

Provide the missing sequences above or adjust the numbering of the sequences and change <160> to reflect the actual total.


\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

Application No: 10709572

Version No:     1.0

**Started:**  2007-04-26 15:09:46.706
**Finished:**  2007-04-26 18:23:53.100
**Elapsed:**  3 hr(s) 14 min(s) 6 sec(s) 394 ms
**Total Warnings:**  0
**Total Errors:**  75
**No. of SeqIDs Defined:**  10068324
**Actual SeqID Count:**  10068237

| ErrCode | Error Description |
|---------|------------------|
| E  212 | Invalid Sequence ID Number; Expected 165602 as next SeqID but skipped to 165603 |
| E  212 | Invalid Sequence ID Number; Expected 329702 as next SeqID but skipped to 329703 |
| E  212 | Invalid Sequence ID Number; Expected 493802 as next SeqID but skipped to 493803 |
| E  212 | Invalid Sequence ID Number; Expected 657902 as next SeqID but skipped to 657903 |
| E  212 | Invalid Sequence ID Number; Expected 822002 as next SeqID but skipped to 822003 |
| E  212 | Invalid Sequence ID Number; Expected 986102 as next SeqID but skipped to 986103 |
| E  212 | Invalid Sequence ID Number; Expected 1148302 as next SeqID but skipped to 1148303 |
| E  212 | Invalid Sequence ID Number; Expected 1310302 as next SeqID but skipped to 1310303 |
| E  212 | Invalid Sequence ID Number; Expected 1472302 as next SeqID but skipped to 1472303 |
| E  212 | Invalid Sequence ID Number; Expected 1634302 as next SeqID but skipped to 1634303 |
| E  212 | Invalid Sequence ID Number; Expected 1796302 as next SeqID but skipped to 1796303 |
| E  212 | Invalid Sequence ID Number; Expected 1958302 as next SeqID but skipped to 1958303 |
| E  212 | Invalid Sequence ID Number; Expected 2120302 as next SeqID but skipped to 2120303 |
| E  212 | Invalid Sequence ID Number; Expected 2282302 as next SeqID but skipped to 2282303 |

```
        Started:   2007-04-26 15:09:46.706
       Finished:   2007-04-26 18:23:53.100
        Elapsed:   3 hr(s) 14 min(s) 6 sec(s) 394 ms
 Total Warnings:   0
   Total Errors:   75
No. of SeqIDs Defined:   10068324
  Actual SeqID Count:    10068237


ErrCode          Error Description


E  212           Invalid Sequence ID Number; Expected 2444302 as next SeqID but
                 skipped to 2444303

E  212           Invalid Sequence ID Number; Expected 2606302 as next SeqID but
                 skipped to 2606303

E  212           Invalid Sequence ID Number; Expected 2768302 as next SeqID but
                 skipped to 2768303

E  212           Invalid Sequence ID Number; Expected 2930302 as next SeqID but
                 skipped to 2930303

E  212           Invalid Sequence ID Number; Expected 3092302 as next SeqID but
                 skipped to 3092303

E  212           Invalid Sequence ID Number; Expected 3254302 as next SeqID but
                 skipped to 3254303
                  This error has occured more than 20 times, will not be displayed

E  254           The total number of bases conflicts with running total, Input: 22,
                 Calculated : 17 SEQID(6710511)

E  253           The number of bases differs from <211>  Input: 12  Calculated:17
                 SEQID (6710511)

E  254           The total number of bases conflicts with running total, Input: 22,
                 Calculated : 24 SEQID(9319192)

E  253           The number of bases differs from <211>  Input: 22  Calculated:24
                 SEQID (9319192)

E  202           Invalid input format; Value must be an integerin <210> in SEQID
                 (9974642)

E  249           Order Sequence Error <210> -> <213>; Expected Mandatory Tag: <211>
                 in SEQID ( 9974642 )

E  254           The total number of bases conflicts with running total  Input: 0,
                 Calculated : 20 SEQID(10068324)

E  253           The number of bases differs from <211>  Input: 18  Calculated:20
                 SEQID (10068324)

E  252           Calc# of Seq. differs from actual; 10068324 seqIds defined;
                 count=10068237

E  250           Structural Validation Error; Sequence listing may not be indexable
```

<110> ROSETTA GENOMICS LTD
     Bentwich, Itzhak
     Avniel, Amir

<120> BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
     OLIGONUCLEOTIDES AND USES THEREOF

<130> 050992.0202.CPUS01

<140> 10/709,572
<141> 2004-05-14

<160> 10068324

<170> PatentIn version 3.3

<210> 1
<211> 17
<212> DNA
<213> Homo sapiens

<400> 1
gcgcctgtgc ctcctaa                                    17


<210> 2
<211> 22
<212> DNA
<213> Homo sapiens

<400> 2
gctcccactg ctgtcctgcc at                              22


<210> 3
<211> 22
<212> DNA
<213> Homo sapiens

<400> 3

gctgcacttc agcctgggtg tc                                    22


<210> 4
<211> 22
<212> DNA
<213> Homo sapiens

<400> 4
gctggctcca cctgctgcca gg                                    22


<210> 5
<211> 21
<212> DNA
<213> Homo sapiens

<400> 5
ggaatggtgg ttgtatggtt g                                     21


<210> 6
<211> 23
<212> DNA
<213> Homo sapiens

<400> 6
ggccaagtgg atgctggttt agc                                   23


<210> 7
<211> 22
<212> DNA
<213> Homo sapiens

<400> 7
ggccgggtgc tctggaggtg ct                                    22


<210> 8
<211> 22
<212> DNA
<213> Homo sapiens

<400> 8

ggccgtggtc gctgactctc gt                                    22


<210> 9
<211> 22
<212> DNA
<213> Homo sapiens

<400> 9

ggctggttag atttgtggtc tt                                    22


<210> 10
<211> 22
<212> DNA
<213> Homo sapiens

<400> 10

gggaaataat taatgtgaag tc                                    22


<210> 11
<211> 22
<212> DNA
<213> Homo sapiens

<400> 11

ggggaacgcg ctggcccgcg cc                                    22


<210> 12
<211> 19
<212> DNA
<213> Homo sapiens

<400> 12

gggtctctgt tggcttctt                                        19


<210> 13
<211> 22

<212> DNA
<213> Homo sapiens

<400> 13
gggttactct gtgttggtca gg                    22


<210> 14
<211> 22
<212> DNA
<213> Homo sapiens

<400> 14
ggtggcccct gggagatgct gg                    22


<210> 15
<211> 22
<212> DNA
<213> Homo sapiens

<400> 15
gtcagtcatt gaatgctggc ct                    22


<210> 16
<211> 22
<212> DNA
<213> Homo sapiens

<400> 16
gtgcggcctg gccttcaagt gg                    22


<210> 17
<211> 22
<212> DNA
<213> Homo sapiens

<400> 17
gtgcttaaag aatggctgtc cg                    22

<210> 18
<211> 19
<212> DNA
<213> Homo sapiens

<400> 18
gtttctctgg gcttggcat                                          19


<210> 19
<211> 20
<212> DNA
<213> Homo sapiens

<400> 19
tagcatggct ctatggaaca                                         20


<210> 20
<211> 22
<212> DNA
<213> Homo sapiens

<400> 20
taggtatggc ttgtggcaca gc                                      22


<210> 21
<211> 22
<212> DNA
<213> Homo sapiens

<400> 21
tattcattgc ccatgtttgt ga                                      22


<210> 22
<211> 22
<212> DNA
<213> Homo sapiens

<400> 22
tcactgcaac ctccaccttc ag                                      22

<210> 23
<211> 22
<212> DNA
<213> Homo sapiens

<400> 23
tccagctgtc cacgtcttcc tg                                22


<210> 24
<211> 23
<212> DNA
<213> Homo sapiens

<400> 24
tccaggccct caatccattt cca                               23


<210> 25
<211> 22
<212> DNA
<213> Homo sapiens

<400> 25
tcccagctcc tgggccccac ag                                22


<210> 26
<211> 22
<212> DNA
<213> Homo sapiens

<400> 26
tccttcctct gtcaggcagg cc                                22


<210> 27
<211> 22
<212> DNA
<213> Homo sapiens